

RA Rader K.A., Orlando R.A., Lou X., Farquhar M.G.;
 RT "Characterization of ANKRA, a novel ankyrin repeat protein that
 RL interacts with the cytoplasmic domain of megalin.";
 J. Am. Soc. Nephrol. 11:0-0(2001).
 [15]
 RP SEQUENCE FROM N.A.
 RC TISSUE=KIDNEY;
 RA Strasserberg R.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AK022876; BAB1288.1; -.
 DR EMBL; AF251051; AAK3941.1; -.
 DR EMBL; AF34032; AAK01621.1; -.
 DR EMBL; BC012917; AAH12917.1; -.
 DR HSSP; P80144; 2MVO.
 DR InterPro; IPR002110; ANK.
 DR Pfam; PF00023; ank; 3.
 DR PRINTS; PR01415; ANKRYIN.
 DR SMART; SM00248; ANK; 3.
 DR PROSITE; PS50088; ANK_REPEAT; 3.
 DR PROSITE; PS50089; ANK_REGION; 1.
 KW ANK repeat; Hypothetical protein; Repeat.
 SEQUENCE 313 AA; 34272 MW; 3B52B1415B7A5AFA CRC64;

Query Match Best Local Similarity 46.3%; Score 621.5; DB 4; Length 313;
 Matches 60.6%; Pred. No. 2; g-e-44; Indels 49; Gaps 7; Gaps 2;
 保守性 26; Mismatches 49; Indels 7; Gaps 2;

QY 51 NPERDASV-----SSPQAGSSLKHSTTLNRQGENEVSALPATLDSLSHOLAAGELD 104
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Do 104 SPSPGIVQRHVYTSTKHSPIKOSTTILNKHRGENVSTPLANSLSHQAGEML 163
 QY 105 OLKEHLRKGDNNLVNPKDERGFTPLIWASAFGEIETVRFLLEGDPHILAKERESLSLA 164
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 164 YLATRIEQ-ENVINHTDEEGFTPLWAAHQAWEFLONGADPQLGKGRESALSLA 222
 QY 165 STGGYTDIVGLLRRDVNIYDNGGTPLYAVYRGNHVCKVCKMLLESADPTIEDSGY 224
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Do 223 CSKGTYTDIVKMLLDCGVDNBYDNGGTPLYAVYRGNHVCKVCKMLLESADPTIEDSGY 282
 QY 225 TPMDLAVLAGYRKVQQVTEHNILKLQFOS 252
 :|||:|||:|||:|||:|||:|||:
 Db 283 NSMDLAVLAGYRKVQQVTEHNILKLQFOS 310

RESULT 2
 Q99PE2 PRELIMINARY; PRT; 312 AA.
 AC Q99PE2; ID 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DE Ankyrin-repeat family A protein.
 GN ANKRA2 OR 1110004M18RK.
 OS Mus musculus (Mouse).
 OC Bokuyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=109090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; PRELIMINARY; PRT; 154 AA.
 RX MEDLINE=21085650; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I.,
 RA Saito T., Otsuka Y., Gojobori T., Boni H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blaize J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M.,
 RA Gustincich S., Hill D., Hoffmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez L., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibusawa Y., Storch K.-F.,
 RA Suzuki H., Tovo-Oka, Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohitsuki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:695-697(2001).
 DR EMBL; AK003438; BAB22790.1; -.
 DR HSSP; P80144; 2MVO.
 DR MGD; MGI-191808; Ankra2.
 DR InterPro; IPR002110; ANK.

QY 51 NPERDASV-----SSPQAGSSLKHSTTLNRQGENEVSALPATLDSLSHOLAAGELD 104
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Do 103 SPSPGIVQRHVYTSTKHSPIKOSTTILNKHRGENVSTPLANSLSHQAGEML 162
 QY 105 OLKEHLRKGDNNLVNPKDERGFTPLIWASAFGEIETVRFLLEGDPHILAKERESLSLA 164
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 163 YLATRIEQ-ENVINHTDEEGFTPLWAAHQAWEFLONGADPQLGKGRESALSLA 221
 QY 165 STGGYTDIVGLLRRDVNIYDNGGTPLYAVYRGNHVCKVCKMLLESADPTIEDSGY 224
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Do 222 CSKGTYTDIVKMLLDCGVDNBYDNGGTPLYAVYRGNHVCKVCKMLLESADPTIEDSGY 281
 QY 225 TPMDLAVLAGYRKVQQVTEHNILKLQFOS 252
 :|||:|||:|||:|||:
 Do 282 NSMDLAVLAGYRKVQQVTEHNILKLQFOS 309

RESULT 3
 Q99PE2 PRELIMINARY; PRT; 154 AA.
 AC Q99PE2; ID 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 21, Last annotation update)
 DE 1110004M18RK protein.
 GN ANKRA2 OR 1110004M18RK.
 OS Mus musculus (Mouse).
 OC Bokuyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=109090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; PRELIMINARY; PRT; 154 AA.
 RX MEDLINE=21085650; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I.,
 RA Saito T., Otsuka Y., Gojobori T., Boni H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blaize J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M.,
 RA Gustincich S., Hill D., Hoffmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez L., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibusawa Y., Storch K.-F.,
 RA Suzuki H., Tovo-Oka, Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohitsuki S.,
 RA Hayashizaki Y.,
 RT "Characterization of ANKRA, a novel ankyrin repeat protein that
 interacts with the cytoplasmic domain of megalin.";
 J. Am. Soc. Nephrol. 11:2167-2178(2000).
 DR EMBL; AF314031; AAK01620.1; -.

DR pFam; PR00023; ank; 3.
 DR PRINTS; PR01415; ANKYRIN.
 DR SMART; SM00248; ANK; 3.
 DR PROSITE; PS50088; ANK_REPEAT; 3.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 DR ANK_repeat; Repeat; 154 AA; 16701 MW; 95E66FF4CF0B069A CRC64;
 SQ SEQUENCE 32.7%; Score 439; DB 11; Length 154;
 Best Local Similarity 68.3%; Pred. No. 2. 4e-29;
 Matches 84; Conservative 13; Mismatches 26; Indels 0; Gaps 0;
 RT Science 287:2185-2195(2000).
 RN [2]
 RP STRAIN=BERKELEY;
 RC Stapleton M., Brokstein P., Hong L., Aqbayani A., Carlson J.,
 RA Champé M., Chavez C., Dorsett V., Fartan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mongail C.J.,
 RA Munoz J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003626; AAU52838.2; -.
 DR EMBL; AE061547; AAU29095.1; -.
 DR HSSP; PR0144; 2M0C.
 DR FlyBase; FBgn0032171; CG5846.
 DR InterPro; IPR002110; ANK.
 DR Pfam; PF00023; ank; 4.
 DR PRINTS; PR01415; ANKYRIN.
 DR SMART; SM00248; ANK; 3.
 DR PROSITE; PS50088; ANK_REPEAT; 2.
 DR PRINTS; PR01415; ANK; 3.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 SQ SEQUENCE FROM N.A.
 RESULT 4
 Q9VLS8 PRELIMINARY; PRT; 234 AA.
 AC Q9VLS8;
 DT 01-MAY-2000 (T+EMBLrel. 13, Created)
 DT 01-JUN-2002 (T+EMBLrel. 21, Last annotation update)
 DE CG5846 protein (LP07441p).
 GN CG5846.
 OC Drosophila melanogaster (Fruit fly).
 OC Drosophila; Metarco; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydioidea; Drosophilidae; Drosophila.
 RN [1]
 RP STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ammariades P.G., Scheer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Baezaj R.G., Channe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
 RA Abil J.F., Agbanya A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokschein P., Brottier P.,
 RA Burtis K.C., Buseman D.A., Butler H., Cadieu E., Center A., Chanda I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA De Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dierz S.M.,
 RA Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin R.K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Garg N.S., Gebart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levintsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mathei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mohrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Purvi V., Reese M.G.,
 RA Reineert K., Remington K., Saunders D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpers M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhou M., Zhang G., Zhao Q., Zheng L.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC Stapleton M., Brokstein P., Hong L., Aqbayani A., Carlson J.,
 RA Champé M., Chavez C., Dorsett V., Fartan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mongail C.J.,
 RA Munoz J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003626; AAU52838.2; -.
 DR EMBL; AE061547; AAU29095.1; -.
 DR HSSP; PR0144; 2M0C.
 DR FlyBase; FBgn0032171; CG5846.
 DR InterPro; IPR002110; ANK.
 DR Pfam; PF00023; ank; 4.
 DR PRINTS; PR01415; ANKYRIN.
 DR SMART; SM00248; ANK; 3.
 DR PROSITE; PS50088; ANK_REPEAT; 2.
 DR PRINTS; PR01415; ANK; 3.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 SQ SEQUENCE 20.4%; Score 274; DB 5; Length 234;
 Best Local Similarity 33.8%; Pred. No. 3. 6e-15; Mismatches 96; Indels 24; Gaps 6;
 Matches 80; Conservative 37; Mismatches 96; Indels 24; Gaps 6;
 RT Query Match 20.4%; Score 274; DB 5; Length 234;
 Best Local Similarity 33.8%; Pred. No. 3. 6e-15; Mismatches 96; Indels 24; Gaps 6;
 Matches 80; Conservative 37; Mismatches 96; Indels 24; Gaps 6;
 SQ SEQUENCE FROM N.A.
 RESULT 5
 Q8YTG9 PRELIMINARY; PRT; 426 AA.
 AC Q8YTG9;
 DT 01-MAR-2002 (T+EMBLrel. 20, Created)
 DT 01-MAR-2002 (T+EMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (T+EMBLrel. 21, Last annotation update)
 DE Hypothetical protein All2748.
 GN All2748.
 OS *Anabaena* sp. (strain PCC 7120).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
 OX NCBI_TaxId=103690;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21595205; PubMed=11759840;
 RA Kaneko T., Nakamura Y., Wakaku C.P., Kuritz T., Sasamoto S.,
 RA Yamada A., Iriuchi M., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kohara M., Matsunoto M., Mattano A., Miraki A.,
 RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
 RA Yasuda M., Tabata S.;
 RT "Complete genomic sequence of the filamentous nitrogen-fixing
 cyanobacterium *Anabaena* sp. strain PCC 7120.";

RL	DNA Res.	8:205-213 (2001).	SQ	SEQUENCE	1786 AA:	195550 MW;	03E220FB521747F1 CRC64;
DR	EMBL; AP003590; BAB4447.1; -.	Query Match	16.0 %;	Score	214;	DB 5;	Length 1786;
DR	InterPro; IPR002110; ANK.	Best Local Similarity	27.3 %;	Pred.	No. 8.7e-09;		
DR	Pfam; PF00023; ank; 13.	Matches	62;	Conservative	36;	Mismatches	87;
DR	PRINTS; PR01415; ANKTRIN.	Indels	42;	Gaps			4;
DR	SMART; SM00248; ANK; 13.	Score	21.95;	DB	16;	Length	426;
DR	PROSITE; PS50088; ANK_REPEAT; 11.	Best local Similarity	30.7 %;	Pred.	No. 3.5e-10;		
DR	PROSITE; PS50297; ANK REP REGION; 1.	Matches	62;	Conservative	34;	Mismatches	71;
KW	Hypothetical protein; Complete proteome.	Indels	35;	Gaps	4;		
SQ	SEQUENCE	426 AA;	43800 MW;	CFOB925D43ACAA03	CRC64;		
Query Match	16.4 %;	Score	219.5;	DB	16;	Length	426;
Best local Similarity	30.7 %;	Pred.	No. 3.5e-10;				
Matches	62;	Conservative	34;	Mismatches	71;	Indels	35;
DR	PROSITE; PS50088; ANK_REPEAT; 11.	Gaps	4;				
Qy	62 QAGSSLKHSTTL-----TNRQNEVSAALPATDSLTHOLANQELDQIK 107	Score	214;	DB	5;	Length	1786;
Db	234 QDGESALHATVEGVYDVQVLLNQGANTQINKLKGTLPLVLAQOIV-----DOI 285	Best Local Similarity	27.3 %;	Pred.	No. 8.7e-09;		
Qy	108 EHURK---GDNLVNKPDERGFPLIWAISAFGEIETVRFLEWGADPHILAKERESAL 161	Matches	62;	Conservative	36;	Mismatches	87;
Db	286 ETILKYGANVHGDLN----GETPLTLAASQHTATVIRLTDYGANANIPASDGITAL 338	Indels	42;	Gaps			4;
Qy	162 SLASTGGYDIVGLLRLRDVNIYVWNGGFLPLIAYVRGNHVKCVAEALLARGADLTREAD 221	Score	219.5;	DB	16;	Length	426;
Db	339 IKATERNHQVITOLLAKGANYQDSVGATAHLIWAASGGYKVNQVILEGGADTNKRN 398	Best local Similarity	30.7 %;	Pred.	No. 3.5e-10;		
Qy	222 SGYTPMDLAVALGYKVQVQIE 243	Matches	62;	Conservative	34;	Mismatches	71;
Db	399 GGTYALMMAEFNGFFRSIVQIIC 420	Indels	35;	Gaps	4;		
RESULT 6							
ID	Q17344	PRELIMINARY;	PRT;	1786 AA.			
AC	Q17344;						
DT	01-NOV-1996 (TREMBREL 01; Last sequence update)						
DT	01-MAR-2002 (TREMBREL 20; Last annotation update)						
DE	UNC-44 (Fragment).						
OS	Caenorhabditis elegans.						
OC	Rhabditida; Peioderinae; Caenorhabditis.						
OX	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;						
NCBI_TaxID	6239;						
RP	SEQUENCE FROM N.A.						
RX	MEDLINE=94150718; PubMed=7906398;						
RA	Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A.,						
RA	Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,						
RA	Craxton M., Dear S., Du S., Durbin R., Favello A., Fulton L.,						
RA	Gardiner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,						
RA	Jones M., Kershaw J., Kirsten J., Laster N., Latreille P.,						
RA	Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,						
RA	Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showrikeen R.,						
RA	Smalton N., Smith A., Sonnhammer E., Staden R., Sulston J.,						
RA	Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Watson R.,						
RA	Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,						
RT	"An ankyrin-related gene (unc-44) is necessary for proper axonal						
RT	guidance in Caenorhabditis elegans.";						
RL	J. Cell Biol. 129:1061-1092 (1995).						
DR	EMBL; U21734; AAA05854.1; _.						
DR	HSSP; P42773; 1IB.						
DR	InterPro; IPR002110; ANK.						
DR	InterPro; IPR000488; Death.						
DR	SMART; SM00005; DEATH; 1.						
DR	InterPro; IPR000906; ZU5.						
DR	PFam; PF00023; ank; 24.						
DR	Pfam; PF00531; death; 1.						
DR	PROSITE; PS50297; ANK REP REGION; 1.						
DR	PROSITE; PS50017; DEATH DOMAIN; 1.						
DR	PROSITE; PS50572; GLYCOSYL_HYDROL_FL1; UNKNOWN_2.						
KW	ANK repeat; Repeat.						
FT	NON_TER						
	1786						

DR SMART; SW00218; ZU5; 1.
 DR PROSITE; PS5088; ANK REPEAT; 22;
 DR PROSITE; PS50297; ANK REP REGION; 1.
 DR PROSITE; PS50017; DEATH DOMAIN; 1.
 DR PROSITE; PS05372; GLYCOSYL_HYDROL_F1_1; UNKNOWN_2.
 KW ANK repeat; Repeat; 1809 AA; 198193 MW; AD86349A64534F8 CRC64;
 SQ SEQUENCE FROM N.A.

Query	Match	Score	DB	Length	Best Local Similarity	Pred.	No.	Mismatches	Indels	Gaps
QY 19 SELGDPEDPGEEAADGSDTIVVLSLFCCTPEPVNPEDAVSSPQAGSSLKISTTLNQR	16.0%	214	5	1809	27.3%	8	9e-09			
Db 2 SNEGPPQQQQQQPESQVA---PAAPEGRAE-----					36					
QY 79 GNEVALPATLDSLTHQLAAQEGELDOLKEURKGDNVLNKDERGTPLIWASAFGEIE	138				33					
Db 33 -----GSASFRLRAARGADLEKVLERLAGTD-INTSNANGNLNSHLASKEGHSE	80									
Qy 139 TVRFLIEWGADPHILAKERESALSLASTGGYDIVGILLERDVIDINTDWNGCTPLIYAV	198									
Db 81 VVERELIKRQAQDAATRKGNNTALHTIASLAGSLLIVTENGANVNQSVNGTIPLYMA	140									
QY 199 RGNHVKCYPEALLARGADLTTEADSGYPMIDLAVALGY-RKVQQVIEN 244										
Db 141 QENHEEVVKYLUKKGANOALSTEDGFTPLAVALQGHDWRVAVLEN 187										

RESULT 8

Q17488 PRELIMINARY; PRT; 1815 AA.

ID 017488; 002517;

AC DT 01-NOV-1996 (TREMBREL_01, Created)

DT 01-NOV-1996 (TREMBREL_01, Last sequence update)

DT 01-MAR-2002 (TREMBREL_20, Last annotation update)

DE C_ELEGANS ankyrin-related, 20, UNC-44 (GB:U21734).

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditoidea; Rhabditida; Peloridinae; Caenorhabditida.

OX NCBI_TaxID=239;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94150718; PubMed=7906398;

RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,

RA Field J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,

RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,

RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,

RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,

RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,

RA Parsons J., Percy C., Riftken L., Roopra A., Saunders D., Showmanneen R.,

RA Shadlon N., Smith A., Sonhammer E., Staden R., Sulston J.,

RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,

RA Watson A., Weinstock L., Wilkinson-Spratt J., Wondolowski P., Waterston R.,

RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans." 368:32-38 (1994).

RN [2]

RP SEQUENCE FROM N.A.

RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Waterston R.;

RA Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RN STRAIN=N2;

RX MEDLINE=95263663; PubMed=7744957;

RA Otsuka A.-J., Franco R., Yang B., Shim K., Tang L.Z., Zhang Y., Wheaton V.I.,

RA Boontrakulpoontawee P., Jayaprakash A., Hedgecock E., Wheaton V.I.,

RA Soberly A.;

RT "An ankyrin-related gene (unc-44) is necessary for proper axonal guidance in *Caenorhabditis elegans*." J. Cell Biol. 129:1081-1092(1995).

RN [5]

RP SEQUENCE FROM N.A..

RC STRAIN=N2;

RA Otsuka A.J.;

RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.

RN [6]

RP SEQUENCE FROM N.A..

RC STRAIN=N2;

RA Otsuka A.J.;

RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.

RN [7]

EMBL; U50071; AAA93445.1; -

EMBL; U39847; AAB41826.1; -

HSSP; P42773; I1HB.

DR InterPro; IPR002110; ANK.

DR InterPro; IPR00488; Death.

DR InterPro; IPR001360; GH_1.

DR InterPro; IPR000906; ZU5.

DR Pfam; PF00023; ank; 24.

DR Pfam; PF00531; death; 1.

DR PRINTS; PR01415; ANKYRIN.

DR SMART; SW00248; ANK; 21.

DR SMART; SW00005; DEATH; 1.

DR SMART; SW0018; ZU5; 1.

DR PROSITE; PS5008; ANK REP REPEAT; 22.

DR PROSITE; PS50017; DEATH DOMAIN; 1.

DR PROSITE; PS50017; GLYCOSYL_HYDROL_F1_1; UNKNOWN_2.

KW ANK repeat; Repeat; 1815 AA; 198956 MW; 3ECC6E310915C915 CRC64;

SQ SEQUENCE FROM N.A.

Query Match Score 16.0%; DB 5; Length 1815; Best Local Similarity 27.3%; Pred. No. 8 9e-09; Indels 42; Gaps 4; Mismatches 62; Conservative 36; Mismatches 87; Indels 42; Gaps 4; Matches 62; Conservative 36; Mismatches 87; Indels 42; Gaps 4;

QY 19 SELGDPEDPGEEAADGSDTIVVLSLFCCTPEPVNPEDAVSSPQAGSSLKISTTLNQR
 78 | | | | | | | | | || Db 33 -----GSASFRLRAARGADLEKVLERLAGTD-INTSNANGNLNSHLASKEGHSE | 80 | | | | | | | | | |
Qy 139 TVRFLIEWGADPHILAKERESALSLASTGGYDIVGILLERDVIDINTDWNGCTPLIYAV	198									
Db 81 VVERELIKRQAQDAATRKGNNTALHTIASLAGSLLIVTENGANVNQSVNGTIPLYMA	140									
QY 199 RGNHVKCYPEALLARGADLTTEADSGYPMIDLAVALGY-RKVQQVIEN 244										
Db 141 QENHEEVVKYLUKKGANOALSTEDGFTPLAVALQGHDWRVAVLEN 187										

RESULT 9

Q17486 PRELIMINARY; PRT; 1867 AA.

ID 017486; 002516;

AC DT 01-NOV-1996 (TREMBREL_01, Created)

DT 01-NOV-1996 (TREMBREL_01, Last sequence update)

DT 01-MAR-2002 (TREMBREL_20, Last annotation update)

DE C_ELEGANS ankyrin-related, 20, UNC-44 (GB:U21734).

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditoidea; Rhabditida; Peloridinae; Caenorhabditida.

OX NCBI_TaxID=239;

[1]

RP SEQUENCE FROM N.A..

RX MEDLINE=94150718; PubMed=7906398;

RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,

RA Field J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,

RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,

RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifkin L., Roopa A., Saunders D., Showmankeen R.,
 RA Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
 RA Thiverry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans.";
 RL Nature 368:32-38(1994).
 RN [12]
 RP SEQUENCE FROM N.A.
 RA Gattung S.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Waterston R.;
 RL Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=N2;
 RX MEDLINE=95263663; PubMed=7744957;
 RA Osbuka A.J., Franco R., Yang B., Shim K., Tang L.Z., Zhang Y.,
 RA Boonrakulpoontawee P., Jeyaprakash A., Hedgecock E., Wheaton V.I.,
 RA Sobey A.;
 RT "An ankyrin-related gene (unc-44) is necessary for proper axonal
 guidance in *Caenorhabditis elegans".*
 RL Cell Biol. 129:1081-1092(1995).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=N2;
 RA Otsuba A.J.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=N2;
 RA Oeuka A.J.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; U50071; AAA93444.1; -.
 DR EMBL; U59847; AAB41828.1; -.
 DR PFAM; P42773; L1HB.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR01360; GH 1.
 DR InterPro; IPR000906; ZU5.
 DR PFAM; PF00023; ank; 24.
 DR Pfam; PF00531; death; 1.
 DR Prints; PRO1415; ANKYRIN.
 DR SMART; SM00248; ANK; 21.
 DR SMART; SM0018; ZU5; 1.
 DR PROSITE; PS00088; ANK REPEAT; 22.
 DR PROSITE; PS0017; DEATH DOMAIN; 1.
 DR PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; UNKNOWN_2.
 KW Ank repeat;
 SQ SEQUENCE 1867 AA; 204253 MW; 4689A2104623B4C6 CRC64;

Query Match 16.0%; Score 214; DB 5; Length 1867;
 Best Local Similarity 27.3%; Pred. No. 9.3e-09; Matches 62; Conservative 36; Mismatches 87; Indels 42; Gaps 4;

Qy 19 SELGDPDPGEGADGDTWVLSPCTPEPVNPEDASVSSPQAGSSLKHSTLTNRQ 78
 Db 2 SNEGDPPQPOQQQPESQVA---PAPERSHAE----- 32

Query Match 16.0%; Score 214; DB 5; Length 2039;
 Best Local Similarity 27.3%; Pred. No. 1.1e-08; Matches 62; Conservative 36; Mismatches 87; Indels 42; Gaps 4;

Qy 19 GNEVSAILPATLDSLHOLAAQELDDQIKEHLRKGDNLVKPDERGFTPLIWAQAFGE 138
 Db 33 -----GSASFRLAARGAGLEKVLELLRAGTD-INTSWANGLNSLHASKEHSE 80

Qy 139 TVRFLIEWGADPHILAKERESALSLASTGGYTDIVGLILERDWDINTDWNGTPLIXAV 198

RESULT 10
 Q17489 ID 017489 PRELIMINARY; PRT; 2039 AA.
 AC Q17489;
 RA 01-NOV-1996 (TREMBrel. 01, Created)
 DT 01-NOV-1996 (TREMBrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)
 DE C. elegans ankyrin-related unc-44 (GB:U21734).
 UNCP:44
 GN Caenorhabditis elegans.
 OC Eubaryota; Metazoa; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderrina; Caenorhabditis.
 NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Alnscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifkin L., Roopa A., Saunders D., Showmankeen R.,
 RA Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
 RA Thiverry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans.";
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Gattung S.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Waterston R.;
 RL Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; U50071; AAA93443.1; -.
 DR HSSP; P42773; L1HB.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR01360; GH 1.
 DR InterPro; IPR000906; ZU5.
 DR PFAM; PF00023; ank; 24.
 DR PFAM; PF00531; death; 1.
 DR Prints; PRO1415; ANKYRIN.
 DR Prints; PRO1574; TUBBIPROTEIN.
 DR SMART; SM00248; ANK; 21.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00211; ZU5; 1.
 DR PROSITE; PS50088; ANK REPEAT; 22.
 DR PROSITE; PS50297; ANK REP REGION; 1.
 DR PROSITE; PS50017; DEATH DOMAIN; 1.
 DR PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; UNKNOWN_2.
 SQ SEQUENCE 2039 AA; 22250 MW; 7722C422E6ADF668A CRC64;

Query Match 16.0%; Score 214; DB 5; Length 2039;
 Best Local Similarity 27.3%; Pred. No. 1.1e-08; Matches 62; Conservative 36; Mismatches 87; Indels 42; Gaps 4;

Qy 19 SELGDPDPGEADGDTWVLSPCTPEPVNPEDASVSSPQAGSSLKHSTLTNRQ 78

Db	QY	79 GNEVSLAPATDSLTHOLAAQELDQLKEHLRKGDNLUVKPDRGFTPLIWAFAEGEIE 138
Db	QY	33 -----GSASFRLRAARAGDLERKVELLRRAGTD-INTSNANGLNLSHLASKEGHSE 80
Db	QY	139 TVRFLEWGADPHILAKERESALSLASTGGYTDIVGLLERDVIDNIDWNGGTPLYAV 198
Db	QY	199 RGNHVKCVAELLARGADITTEASGYTMDLAVALGY-RKVQQIVEN 244
Db	QY	141 QENHEEVVKYLKHHGANQALSTEDGFTPLAVALQOQHDRVAVILEN 187
RESULT 11		
Q17343	PRELIMINARY;	PRT; 6994 AA.
ID	Q17343	PRELIMINARY; PRT; 6994 AA.
AC	Q17343;	01-NOV-1996 (TREMBREL. 01, Created)
DT	01-JAN-1998 (TREMBREL. 05, Last sequence update)	01-MAR-2002 (TREMBREL. 20, Last annotation update)
DT	01-MAR-2002 (TREMBREL. 20, Last annotation update)	01-JUN-2002 (TREMBREL. 21, Last annotation update)
DE	UNC-44 ankyrins.	UNC-44 ankyrins.
GN	Caenorhabditis elegans.	Caenorhabditis elegans.
OC	Bukayrota; Metarcoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Pelerinae; Caenorhabditis.	Bukayrota; Metarcoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Pelerinae; Caenorhabditis.
OC	NCBI_TAXID=6239;	NCBI_TAXID=6239;
RN	[1]	[1]
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	STRAININ2;	STRAININ2;
RX	MEDLINE=9563663; PubMed=7744957;	MEDLINE=9563663; PubMed=7744957;
RA	Otsuka A.J., Franco R., Yang B., Shim K., Tang L.Z., Zhang Y.,	Otsuka A.J., Franco R., Yang B., Shim K., Tang L.Z., Zhang Y.,
RA	Boontrakulpoontawee P., Jeyaprakash A., Hedgecock E., Wheaton V.I.,	Boontrakulpoontawee P., Jeyaprakash A., Hedgecock E., Wheaton V.I.,
RA	Sobery A.; "An ankyrin related gene (unc-44) is necessary for proper axonal	Sobery A.; "An ankyrin related gene (unc-44) is necessary for proper axonal
RT	guidance in Caenorhabditis elegans.";	guidance in Caenorhabditis elegans.";
RT	J. Cell Biol. 129:1081-1092(1995).	J. Cell Biol. 129:1081-1092(1995).
RL	[2]	[2]
RN	REVISONS, AND SEQUENCE OF 6126-6994 FROM N.A.	REVISONS, AND SEQUENCE OF 6126-6994 FROM N.A.
RC	STRAININ2;	STRAININ2;
RX	Otsuka A.J., Submitted (DBCB-1996) to the EMBL/GenBank/DBJ databases.	Otsuka A.J., Submitted (DBCB-1996) to the EMBL/GenBank/DBJ databases.
RA	EMBL; U39847; AAB1827_1; -.	EMBL; U39847; AAB1827_1; -.
RA	EMBL; U21733; ARB8384_1; -.	EMBL; U21733; ARB8384_1; -.
RA	HSSP; P42773; 1IHB.	HSSP; P42773; 1IHB.
DR	InterPro; IPR002110; ANK.	InterPro; IPR002110; ANK.
DR	InterPro; IPR00488; Death.	InterPro; IPR00488; Death.
DR	InterPro; IPR001360; GH_1.	InterPro; IPR001360; GH_1.
DR	InterPro; IPR002383; GLA_blood.	InterPro; IPR002383; GLA_blood.
DR	InterPro; IPR00096; ZU5.	InterPro; IPR00096; ZU5.
DR	Pfam; PF00022; ank; 24.	Pfam; PF00022; ank; 24.
DR	Pfam; PF00531; death; 1.	Pfam; PF00531; death; 1.
DR	PRINTS; PRO01415; ANKYRIN.	PRINTS; PRO01415; ANKYRIN.
DR	PRINTS; PRO01415; ANKYRIN.	PRINTS; PRO01415; ANKYRIN.
DR	PRINTS; PRO00011; GLABLOOD.	PRINTS; PRO00011; GLABLOOD.
DR	SMART; SMC248; ANK; 21.	SMART; SMC248; ANK; 21.
DR	SMART; SM00055; DEATH; 1.	SMART; SM00055; DEATH; 1.
DR	PROSITE; PS50088; ZU5; 1.	PROSITE; PS50088; ZU5; 1.
DR	PROSITE; PS50397; ANK_REPEAT; 22.	PROSITE; PS50397; ANK_REPEAT; 22.
DR	PROSITE; PS50017; DEATH_DOMAIN; 1.	PROSITE; PS50017; DEATH_DOMAIN; 1.
DR	PROSITE; PS05572; GLYCOSYL_HYDROL_F1_1; UNKNOWN_2.	PROSITE; PS05572; GLYCOSYL_HYDROL_F1_1; UNKNOWN_2.
KW	ANK repeat; Repeat.	ANK repeat; Repeat.
SQ	SEQUENCE: 6994 AA; 773364 MW; 90CB449925D923D CRC64;	SEQUENCE: 6994 AA; 773364 MW; 90CB449925D923D CRC64;
Query Match Best Local Similarity 16.0%; Score 214; DB 5; Length 6994; Matches 62; Conservative 36; Mismatches 87; Indels 42; Gaps 4;		
QY	19 SELGDPDPGEAAGDSPTVVLSPFCTPEVNPEFDASVSSPOAGSSLKHISTTLNQR 78	QY : :
QY	79 GNEVSLAPATDSLTHOLAAQELDQLKEHLRKGDNLUVKPDRGFTPLIWAFAEGEIE 138	QY : :
Db	33 -----GSASFRLRAARAGDLERKVELLRRAGTD-INTSNANGLNLSHLASKEGHSE 80	Db 33 -----GSASFRLRAARAGDLERKVELLRRAGTD-INTSNANGLNLSHLASKEGHSE 80
Db	QY 139 TVRFLEWGADPHILAKERESALSLASTGGYTDIVGLLERDVIDNIDWNGGTPLYAV 198	Db QY 139 TVRFLEWGADPHILAKERESALSLASTGGYTDIVGLLERDVIDNIDWNGGTPLYAV 198
Db	81 VRELLIKVQDAATRKNTALHISLAGQSLIVTENGAVNVQSVNGFTPLYMA 140	Db 81 VRELLIKVQDAATRKNTALHISLAGQSLIVTENGAVNVQSVNGFTPLYMA 140
Db	199 RGNHVKCVAELLARGADITTEASGYTMDLAVALGY-RKVQQIVEN 244	Db 199 RGNHVKCVAELLARGADITTEASGYTMDLAVALGY-RKVQQIVEN 244
Db	QY 141 QENHEEVVKYLKHHGANQALSTEDGFTPLAVALQOQHDRVAVILEN 187	Db 141 QENHEEVVKYLKHHGANQALSTEDGFTPLAVALQOQHDRVAVILEN 187
RESULT 12		
Q9EQG6	PRELIMINARY;	PRT; 1762 AA.
ID	Q9EQG6	PRELIMINARY; PRT; 1762 AA.
AC	Q9EQG6;	01-DEC-2001 (TREMBREL. 16, Created)
DT	01-OCT-2001 (TREMBREL. 18, Last sequence update)	01-MAR-2002 (TREMBREL. 21, Last annotation update)
DT	01-JUN-2002 (TREMBREL. 21, Last annotation update)	DE KIDINS20.
DE	KIDINS20.	GN
OS	Rattus norvegicus (Rat).	OS
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	OC
OC	NCBI_TAXID=10116;	RN
RN	[1]	[1]
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RA	RA	RA
RA	Iglesias T., Cabreiro-Poch N., Mitchell M.P., Naven T.J., Rozengurt E., Schiavo G.; "Identification and cloning of Kidins220, a novel neuronal substrate of protein kinase D"; J. Biol. Chem. 275:40048-40056(2000).	Iglesias T., Cabreiro-Poch N., Mitchell M.P., Naven T.J., Rozengurt E., Schiavo G.; "Identification and cloning of Kidins220, a novel neuronal substrate of protein kinase D"; J. Biol. Chem. 275:40048-40056(2000).
RA	Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.	Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RA	DR	DR
RA	HSSP; P80144; 2MYO.	HSSP; P80144; 2MYO.
DR	InterPro; IPR002110; ANK.	InterPro; IPR002110; ANK.
DR	Pfam; PF00023; ank; 12.	Pfam; PF00023; ank; 12.
DR	PRINTS; PR01415; ANKYRIN.	PRINTS; PR01415; ANKYRIN.
DR	SMART; SM00248; ANK; 21.	SMART; SM00248; ANK; 21.
DR	SMART; SM00055; DEATH; 1.	SMART; SM00055; DEATH; 1.
DR	PROSITE; PS50088; ANK_REPEAT; 22.	PROSITE; PS50088; ANK_REPEAT; 22.
DR	PROSITE; PS50397; ANK REP REGION; 1.	PROSITE; PS50397; ANK REP REGION; 1.
DR	PROSITE; PS50017; DEATH DOMAIN; 1.	PROSITE; PS50017; DEATH DOMAIN; 1.
DR	PROSITE; PS05572; GLYCOSYL_HYDROL_F1_1; UNKNOWN_2.	PROSITE; PS05572; GLYCOSYL_HYDROL_F1_1; UNKNOWN_2.
KW	KW ANK repeat; Repeat.	KW ANK repeat; Repeat.
SQ	SEQUENCE: 1762 AA; 19515 MW; 0CB2689A57F8AE4 CRC64;	SEQUENCE: 1762 AA; 19515 MW; 0CB2689A57F8AE4 CRC64;
QY	100 QGELDQLKEHLRKGDNLUVKPDRGFTPLIWAFAEGEIE 138	QY 100 QGELDQLKEHLRKGDNLUVKPDRGFTPLIWAFAEGEIE 138
Db	81 EGHTHIVEULLKSGLASKEGHSE 80	Db 81 EGHTHIVEULLKSGLASKEGHSE 80
QY	160 ALSASTGGYTDIVGLLERDVIDNIDWNGGTPLYAV 198	QY 160 ALSASTGGYTDIVGLLERDVIDNIDWNGGTPLYAV 198
Db	140 PIWMAAGRGRDHIVILLONGAKVNCSDKIGITPLWMAARKCHLEGCVKHLAMADVQE 199	Db 140 PIWMAAGRGRDHIVILLONGAKVNCSDKIGITPLWMAARKCHLEGCVKHLAMADVQE 199
Qy	220 ADSGVTPMDLAVALGY-RKVQQIVEN 245	Qy 220 ADSGVTPMDLAVALGY-RKVQQIVEN 245
Db	200 GANSMTALIVAVKGYTOSVKELRKN 226	Db 200 GANSMTALIVAVKGYTOSVKELRKN 226
RESULT 13		
Q9ULHO	PRELIMINARY;	PRT; 1777 AA.
ID	Q9ULHO	PRELIMINARY; PRT; 1777 AA.

AC Q9UHQ0;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE KIAA1250 protein (Fragment).
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TAXID=9606;
 RN [1] SEQUENCE FROM N.A.
 RP TISSUE=BRAIN;
 RX MEDLINE=20039619; PubMed=10574462;
 RA Nagase T., Ishikawa K., Kikuno R., Hirosva M., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XV.
 The complete sequences of 100 new cDNA clones from brain which code
 for large proteins in vitro.";
 RT DNA Res. 6:337-345(1999).
 DR EMBL; ABO33076; BAA86564; 2; -.
 DR InterPro; IPR002110; ANK.
 DR Pfam; PF0023; ank; 12.
 DR PRINTS; PRO1415; ANKVRIN.
 DR SMART; SM00248; ANK; 11.
 DR PROSITE; PS50088; ANK_REPEAT; 10.
 DR PROSITE; PS50297; ANK REP REGION; 1.
 KW ANK repeat; Repeat.
 FT NON TER 1
 SQ 1777 AA; 197209 MW; B6505923FB45F143 CRC64;
 Query Match 15.8%; Score 212; DB 4; Length 1777;
 Best Local Similarity 35.4%; Pred. No. 1 3e-08;
 Matches 51; Conservative 33; Mismatches 61; Indels 2; Gaps 2;
 RT
 Ov 100 QGDUDQKLHKRKGPNLVIKPDERFPTPLIWAASFABEIETVRFLLEWGADPH 159
 Db 87 EGRHVIVELLRKCGVNLERH-DMGWTAALMWACYKGRTDVVLILLSHGANPVSFTGLYSV 145
 Ov 160 ALSLASTGGTYDITGULLERDVIDNIDYDMNGGTPLLYAVRGNHVKCWEALLA 211
 Db 146 PIWAAGKRGHADIVHLONGAKVNGCSDKYGTTPWMAARKGHLECVKHLLAMGADVQDE 205
 Ov 220 ADGGTFFPLDLAVALGY-RKVQVIREH 245
 Db 206 GANSMTALIUVAVKGQGYTQSVEKILRN 232
 RESULT 14
 O9NCBP8 PRELIMINARY; PRT; 1159 AA.
 ID O9NCBP8
 AC O9NCBP8;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Ankyrin 2.
 DE Ankyrin 2.
 DR HSPB1 OR CG7462.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila;
 RN NCBI_TaxID=7227;
 RN [1] SEQUENCE FROM N.A.
 RX MEDLINE=20304926; PubMed=10844021;
 RA Bouley M., Tian M.-Z., Paisley K., Shen Y.-C., Malhotra J.D.,
 RA Hortsch M.;
 RT "The Ig-type cell adhesion molecule neuroglin influences the
 stability of neural ankyrin in the Drosophila embryo but not its
 axonal localization."; J Neurosci. 20:4515-4523 (2000).
 DR EMBL; API90625; RAAF73309; 1, -.
 DR HSSP; P42773; 1IHB.
 DR FlyBase; FBgn0017645; Ank2.
 DR FlyBase; FBgn0017645; Ank.

DR InterPro; IPR002110; ANK.
 DR InterPro; IPR000506; ZU5.
 DR Pfam; PF00023; ank; 24.
 DR Pfam; PF00751; ZU5; 1.
 DR SMART; SM00248; ANK; 21.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50088; ANK_REPEAT; 21.
 DR PROSITE; PS50297; ANK REP REGION; 1.
 KW ANK repeat; Repeat.
 SQ SEQUENCE 1159 AA; 125769 MW; 9ED146C9E483DE58 CRC64;
 Query Match 15.7%; Score 210.5; DB 5; Length 1159;
 Best Local Similarity 35.1%; Pred. No. 9e-09;
 Matches 53; Conservative 28; Mismatches 67; Indels 3; Gaps 2;
 RT
 Ov 93 SIHQLAQEGELDQLEKHLRKGNL-VNKPDERFPTPLIWAASFABEIETVRFLLEWGADPH 151
 Db 14 SPLRAAAGRNNIPLRNLK--NNIDINTNSNAGNALHASKOHHIVSELRLGAIVD 71
 Ov 152 IIAKERESALSLASTGGTYDITGULLERDVIDNIDYDMNGGTPLLYAVRGNHVKCWEALLA 211
 Db 72 SATKKGNTALHIIASLAGQEEVVKLLEHNASVNVQSQNGFTPLYMAQENHDAVRLIS 131
 Ov 212 RQADLTTEADSGYTPMOLAVAGYRKYQVI 242
 Db 132 NGANQSLATEDDGFTPLAVAMOOQCHDKVVAL 162

RESULT 15
 O9NH0 PRELIMINARY; PRT; 1599 AA.
 ID O9NH0
 AC O9NH0;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Gene trap ankyrin repeat containing Protein.
 GN GTAR.
 OS Mus musculus (Mouse).
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TAXID=10900;
 RN [1] SEQUENCE FROM N.A.
 DR STRAIN=129/SV;
 RA Watt A.J., Jones E.A., Ure J., Peddie D., Wilson D., Forrester L.M.;
 RT "A gene trap integration provides an early in situ marker for hepatic
 specification of the foregut endoderm.";
 RT Mech. Dev. 100/2:205-215 (2001).
 RL EMBL; AY046253; AAK07672; 1; -.
 DR HSSP; P42773; 1IHB.
 DR MGDB; MG1:1932101; Grar.
 DR InterPro; IPR002110; ANK.
 DR Pfam; PF00023; ank; 25.
 DR PRINTS; PRO1415; ANKVRIN.
 DR SMART; SM00248; ANK; 25.
 DR PROSITE; PS50088; ANK_REPEAT; 20.
 DR PROSITE; PS50297; ANK REP REGION; 1.
 KW ANK repeat; Repeat.
 SQ SEQUENCE 1599 AA; 170271 MW; CCB6C56D8ECB7C8 CRC64;
 Query Match 15.7%; Score 210.5; DB 11; Length 1599;
 Best Local Similarity 29.5%; Pred. No. 1 5e-08;
 Matches 71; Conservative 43; Mismatches 98; Indels 29; Gaps 8;
 RT
 Ov 10 LIQPOQO-----TAPASLGDPDPD---GEEADGSPVWLSPFCPTPEPVNPBDASVSS 60
 Db 999 LRETQGLMWASPAQTLNDTLDIMAVSGRASMSNTPTHSIAASVSPQTOPPSPIS 057
 Ov 61 PQAGSSLKHITLNRQRGHEWSALPATLDSLIHOLAOGELDOLKEHLRKCDNLVNUKP 120
 Db 1058 PSAMUPIYPAIDQAQTESHTDAL-----TLCAGSGHELUVOTLURGASIEHR 1107
 Ov 121 DERGFPTPLIWAASFABEIETVRFLLEWGADPHLA-KERESALSLASTGGTYDITGULLER 179

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Job time : 39 secs

